

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 22:28:09 ; Search time 346.26 Seconds
(without alignments)
4455.758 Million cell updates/sec

Title: US-10-073-123-3
Perfect score: 2973
Sequence: 1 ctggctctgctgcctccgc.....tgaaaaaaaaaaaaaaaaaa 2973

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 8336576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : Published Applications NA New:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	176	5.9	1765	6	US-10-750-185-43043
C 2	58.4	2.0	139054	7	US-11-121-086-96
C 3	54.8	1.8	1082144	7	US-11-117-187-211
C 4	50.6	1.7	173602	7	US-11-121-086-25
C 5	49.2	1.7	171486	7	US-11-121-086-105
C 6	48.6	1.6	119036	6	US-10-995-561-13314
C 7	48.2	1.6	49979	6	US-10-995-561-13443
C 8	48.2	1.6	105550	6	US-10-995-561-12235
C 9	46.6	1.6	4744	6	US-10-750-185-56531
C 10	46.6	1.6	26772	6	US-10-995-561-13313
C 11	46.6	1.6	54946	6	US-10-995-561-13479
C 12	46.4	1.6	1353	6	US-10-750-185-61820
C 13	46.4	1.6	184868	7	US-11-121-086-88
C 14	46	1.5	171486	7	US-11-121-086-105
C 15	45.8	1.5	207908	7	US-11-112-908-21
C 16	45.4	1.5	47572	6	US-10-995-561-13356
C 17	45	1.5	158692	7	US-11-121-086-30
C 18	44.8	1.5	919	6	US-10-750-185-49202
C 19	44.6	1.5	195998	6	US-10-995-561-13489
C 20	44.6	1.5	398287	6	US-10-995-561-13396
C 21	44	1.5	139054	7	US-11-121-086-96
C 22	44	1.5	191684	7	US-11-121-086-2
C 23	43.8	1.5	1457	6	US-10-750-185-59517

C 24	43.6	1.5	201990	6	US-10-995-561-13303	Sequence 13303, A
C 25	43.6	1.5	340000	7	US-11-102-978-3	Sequence 3, Appli
C 26	43.4	1.5	2543	6	US-10-750-185-54942	Sequence 54942, A
C 27	43.4	1.5	105550	6	US-10-995-561-12335	Sequence 13255, A
C 28	43.2	1.5	20317	6	US-10-995-561-13460	Sequence 13460, A
C 29	43.2	1.5	27902	6	US-10-995-561-13462	Sequence 13462, A
C 30	43.2	1.5	65931	6	US-10-995-561-13254	Sequence 13254, A
C 31	43	1.4	173602	7	US-11-121-086-25	Sequence 25, Appli
C 32	42.8	1.4	149419	7	US-11-112-908-49	Sequence 49, Appli
C 33	42.8	1.4	161726	7	US-11-112-908-48	Sequence 48, Appli
C 34	42.8	1.4	161726	7	US-11-112-908-52	Sequence 52, Appli
C 35	42.8	1.4	166111	7	US-11-112-908-47	Sequence 47, Appli
C 36	42.6	1.4	3206	6	US-10-750-185-34773	Sequence 34773, A
C 37	42.6	1.4	317876	6	US-10-995-561-13227	Sequence 13227, A
C 38	42.4	1.4	2156	6	US-10-750-185-51326	Sequence 51326, A
C 39	42.4	1.4	4248	6	US-10-793-626-3669	Sequence 3669, Ap
C 40	42.4	1.4	48203	6	US-10-995-561-13378	Sequence 13378, A
C 41	42.4	1.4	172543	7	US-11-121-086-6	Sequence 6, Appli
C 42	42.2	1.4	1124	7	US-11-186-284-84	Sequence 84, Appli
C 43	42.2	1.4	1426	6	US-10-750-185-37047	Sequence 37047, A
C 44	41.8	1.4	1685	6	US-10-750-185-38619	Sequence 38619, A
C 45	41.8	1.4	103931	7	US-11-117-187-193	Sequence 193, App
C 46	41.6	1.4	193363	7	US-11-112-908-32	Sequence 32, Appli
C 47	41.4	1.4	1372	6	US-10-750-185-53210	Sequence 53210, A
C 48	41.2	1.4	26772	6	US-10-995-561-13313	Sequence 13313, A
C 49	41.2	1.4	54946	6	US-10-995-561-13479	Sequence 13479, A
C 50	41.2	1.4	172543	7	US-11-121-086-6	Sequence 6, Appli
C 51	41	1.4	119036	6	US-10-995-561-13314	Sequence 13314, A
C 52	41	1.4	153376	7	US-11-121-086-5	Sequence 5, Appli
C 53	41	1.4	164810	7	US-11-121-086-4	Sequence 4, Appli
C 54	40.8	1.4	809	6	US-10-750-185-56668	Sequence 56668, A
C 55	40.8	1.4	1287	6	US-10-750-185-41535	Sequence 41535, A
C 56	40.8	1.4	137935	6	US-10-995-561-13278	Sequence 13278, A
C 57	40.6	1.4	1478	6	US-10-750-185-38978	Sequence 38978, A
C 58	40.6	1.4	47444	6	US-10-995-561-13354	Sequence 13354, A
C 59	40.6	1.4	124972	7	US-11-121-086-100	Sequence 100, App
C 60	40.6	1.4	151169	7	US-11-121-086-38	Sequence 38, Appli
C 61	40.6	1.4	611587	7	US-11-117-187-209	Sequence 209, App
C 62	40.4	1.4	201	6	US-10-995-561-38224	Sequence 38224, A
C 63	40.4	1.4	822	7	US-11-196-475-143	Sequence 143, App
C 64	40.4	1.4	98716	6	US-10-995-561-13331	Sequence 13331, A
C 65	40.2	1.4	936	6	US-10-750-185-43199	Sequence 43199, A
C 66	40.2	1.4	1598	6	US-10-750-185-58301	Sequence 58301, A
C 67	40.2	1.4	2121	6	US-10-750-185-55309	Sequence 55309, A
C 68	40	1.3	3721	6	US-10-793-626-3966	Sequence 3966, Ap
C 69	40	1.3	12277	6	US-10-477-507A-3	Sequence 3, Appli
C 70	40	1.3	47444	6	US-10-995-561-13354	Sequence 13354, A
C 71	40	1.3	235033	7	US-11-157-389-1	Sequence 1, Appli
C 72	40	1.3	237326	7	US-11-157-389-2	Sequence 2, Appli
C 73	40	1.3	394468	6	US-10-995-561-13473	Sequence 13473, A
C 74	39.8	1.3	1740	6	US-10-750-185-35247	Sequence 35247, A
C 75	39.8	1.3	3494	6	US-10-750-185-52984	Sequence 52984, A
C 76	39.8	1.3	3619	6	US-10-793-626-3335	Sequence 3335, Ap
C 77	39.8	1.3	38030	6	US-10-793-626-3934	Sequence 3934, Ap
C 78	39.8	1.3	39050	6	US-10-857-780-7	Sequence 7, Appli
C 79	39.8	1.3	180654	7	US-11-121-086-58	Sequence 58, Appli
C 80	39.6	1.3	3043	6	US-10-793-626-4176	Sequence 4176, Ap
C 81	39.6	1.3	3454	6	US-10-793-626-4313	Sequence 4313, Ap
C 82	39.6	1.3	4093	6	US-10-750-185-41042	Sequence 41042, A
C 83	39.6	1.3	173995	6	US-10-995-561-13277	Sequence 13277, A
C 84	39.6	1.3	305312	6	US-10-995-561-13236	Sequence 13236, A
C 85	39.4	1.3	683	7	US-11-112-908-89	Sequence 89, Appli
C 86	39.4	1.3	725	6	US-10-750-185-41060	Sequence 41060, A
C 87	39.4	1.3	733	6	US-10-750-185-49714	Sequence 49714, A
C 88	39.4	1.3	1652	6	US-10-750-185-51324	Sequence 51324, A
C 89	39.4	1.3	5801	7	US-11-000-463-580	Sequence 580, App
C 90	39.4	1.3	180862	7	US-11-112-908-40	Sequence 40, Appli
C 91	39.4	1.3	1082144	7	US-11-117-187-211	Sequence 211, App
C 92	39.2	1.3	1329	6	US-10-750-185-28900	Sequence 28900, A
C 93	39.2	1.3	12277	6	US-10-477-507A-3	Sequence 3, Appli
C 94	39.2	1.3	116856	7	US-11-143-980-1	Sequence 1, Appli
C 95	39	1.3	1104	6	US-10-750-185-34385	Sequence 34385, A
C 96	39	1.3	1350	6	US-10-750-185-44781	Sequence 44781, A

C	97	39	1.3	3330	6	US-10-750-185-61867	A	Sequence 61867, A	c 170	37.4	1.3	124972	7	US-11-121-086-100	Sequence 100, App
C	98	39	1.3	49979	6	US-10-995-561-13443	A	Sequence 13443, A	c 171	37.4	1.3	134499	7	US-11-117-187-192	Sequence 192, App
C	99	38.8	1.3	1098	6	US-10-750-185-42424	A	Sequence 42424, A	c 172	37.4	1.3	156735	7	US-11-121-086-93	Sequence 93, Appl
C	100	38.8	1.3	1200	6	US-10-750-185-53480	A	Sequence 53480, A	c 173	37.4	1.3	170995	7	US-11-121-086-35	Sequence 35, Appl
C	101	38.8	1.3	1433	6	US-10-750-185-27017	A	Sequence 27017, A	c 174	37.4	1.3	190276	6	US-10-661-966-1	Sequence 1, Appl
C	102	38.8	1.3	1881	6	US-10-750-185-39253	A	Sequence 39253, A	c 175	37.2	1.3	742	6	US-10-750-185-45165	Sequence 45165, A
C	103	38.8	1.3	2633	6	US-10-750-185-42856	A	Sequence 42856, A	c 176	37.2	1.3	749	6	US-10-750-185-27021	Sequence 27021, A
C	104	38.8	1.3	3001	7	US-11-145-703-116	App	Sequence 116, App	c 177	37.2	1.3	1041	6	US-10-750-185-52852	Sequence 52852, A
C	105	38.8	1.3	11070	7	US-11-075-185-34	App	Sequence 34, App	c 178	37.2	1.3	1213	6	US-10-750-185-45278	Sequence 45278, A
C	106	38.8	1.3	23257	6	US-10-995-561-13412	A	Sequence 13412, A	c 179	37.2	1.3	1317	7	US-11-196-475-167	Sequence 167, App
C	107	38.8	1.3	78869	6	US-11-075-185-1	App	Sequence 1, App	c 180	37.2	1.3	1356	6	US-10-750-185-50810	Sequence 50810, A
C	108	38.8	1.3	98716	6	US-10-995-561-13331	A	Sequence 13331, A	c 181	37.2	1.3	1342	6	US-10-750-185-32858	Sequence 32858, A
C	109	38.6	1.3	698	6	US-10-750-185-63807	A	Sequence 63807, A	c 182	37.2	1.3	1766	6	US-10-750-185-64570	Sequence 64570, A
C	110	38.6	1.3	990	6	US-10-750-185-54762	A	Sequence 54762, A	c 183	37.2	1.3	1896	6	US-10-750-185-64570	Sequence 64570, A
C	111	38.6	1.3	1106	7	US-11-080-991-29	App	Sequence 29, App	c 184	37.2	1.3	2343	6	US-10-750-185-42759	Sequence 42759, A
C	112	38.6	1.3	1721	6	US-10-750-185-64396	A	Sequence 64396, A	c 185	37.2	1.3	2343	6	US-10-750-185-27033	Sequence 27033, A
C	113	38.6	1.3	2624	6	US-10-750-185-38287	A	Sequence 38287, A	c 186	37.2	1.3	40987	6	US-10-995-561-13503	Sequence 13503, A
C	114	38.6	1.3	2862	6	US-10-793-626-4341	Ap	Sequence 4341, Ap	c 187	37.2	1.3	48000	7	US-11-159-597-20	Sequence 20, Appl
C	115	38.6	1.3	13672	7	US-11-055-035-2	App	Sequence 2, App	c 188	37.2	1.3	85682	7	US-11-117-187-205	Sequence 205, Appl
C	116	38.6	1.3	16914	7	US-10-995-561-13349	A	Sequence 13349, A	c 189	37.2	1.3	184868	7	US-11-121-086-31	Sequence 88, Appl
C	117	38.6	1.3	168656	7	US-11-112-908-59	App	Sequence 59, App	c 190	37.2	1.3	218821	7	US-11-121-086-31	Sequence 23, Appl
C	118	38.6	1.3	170285	7	US-11-112-908-58	App	Sequence 58, App	c 191	37.2	1.3	260209	6	US-10-933-025-23	Sequence 23, Appl
C	119	38.6	1.3	201990	6	US-10-995-561-13303	A	Sequence 13303, A	c 192	37	1.2	755	6	US-10-750-185-47742	Sequence 47742, A
C	120	38.6	1.3	1080000	6	US-10-928-446A-1	Sequence 1, App	Sequence 1, App	c 193	37	1.2	990	6	US-10-750-185-30177	Sequence 30177, A
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C	122	38.6	1.3	1080000	6	US-10-928-446A-183	App	Sequence 183, App	c 195	37	1.2	1033	6	US-10-750-185-51040	Sequence 51040, A
C	123	38.6	1.3	1080000	6	US-10-928-446A-185	App	Sequence 185, App	c 196	37	1.2	1063	6	US-10-750-185-48014	Sequence 48014, A
C	124	38.6	1.3	1080000	6	US-10-928-446A-187	App	Sequence 187, App	c 197	37	1.2	1208	6	US-10-750-185-48532	Sequence 48532, A
C	125	38.6	1.3	1080000	6	US-10-928-446A-189	App	Sequence 189, App	c 198	37	1.2	1825	6	US-10-750-185-39541	Sequence 39541, A
C	126	38.6	1.3	1080000	6	US-10-928-446A-191	App	Sequence 191, App	c 199	37	1.2	1919	6	US-10-415-198A-14	Sequence 14, Appl
C	127	38.6	1.3	1080000	6	US-10-928-446A-193	App	Sequence 193, App	c 200	37	1.2	2496	6	US-10-750-185-36044	Sequence 36044, A
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C	129	38.6	1.3	1080000	6	US-10-928-446A-197	App	Sequence 197, App							
C	130	38.6	1.3	1080000	6	US-10-928-446A-199	App	Sequence 199, App							
C	131	38.6	1.3	1080000	6	US-10-928-446A-201	App	Sequence 201, App							
C	132	38.4	1.3	2457	6	US-10-955-054A-102	App	Sequence 102, App							
C	133	38.4	1.3	4675	6	US-10-750-185-28612	A	Sequence 28612, A							
C	134	38.4	1.3	151169	7	US-11-121-086-38	App	Sequence 38, App							
C	135	38.4	1.3	161874	7	US-11-121-086-75	App	Sequence 75, App							
C	136	38.2	1.3	201	6	US-10-995-561-73235	A	Sequence 73235, A							
C	137	38.2	1.3	822	7	US-11-196-475-141	App	Sequence 141, App							
C	138	38.2	1.3	2584	6	US-10-821-234-836	App	Sequence 836, App							
C	139	38.2	1.3	3075	7	US-11-194-246-134	App	Sequence 134, App							
C	140	38.2	1.3	398287	6	US-10-995-561-13396	A	Sequence 13396, A							
C	141	38.2	1.3	645179	6	US-10-995-561-13293	A	Sequence 13293, A							
C	142	38	1.3	951	6	US-10-750-185-49829	A	Sequence 49829, A							
C	143	38	1.3	1017	6	US-10-750-185-56417	A	Sequence 56417, A							
C	144	38	1.3	1588	6	US-10-750-185-27938	A	Sequence 27938, A							
C	145	38	1.3	1781	6	US-10-750-185-64701	A	Sequence 64701, A							
C	146	38	1.3	2597	6	US-10-750-185-44726	A	Sequence 44726, A							
C	147	37.8	1.3	2091	6	US-10-995-561-73234	A	Sequence 73234, A							
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C	153	37.8	1.3	44848	7	US-11-106-672A-42	App	Sequence 42, App							
C	154	37.8	1.3	76589	6	US-10-995-561-13322	A	Sequence 13322, A							
C	155	37.8	1.3	160213	7	US-11-121-086-103	App	Sequence 103, App							
C	156	37.8	1.3	163317	7	US-11-117-187-212	App	Sequence 212, App							
C	157	37.8	1.3	191343	7	US-11-112-908-53	App	Sequence 53, App							
C	158	37.6	1.3	2023	6	US-10-995-561-204	App	Sequence 55, App							
C	159	37.6	1.3	3001	7	US-11-145-703-204	App	Sequence 204, App							
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C	162	37.6	1.3	40439	6	US-10-995-561-13233	A	Sequence 1, Appl							
C	163	37.6	1.3	199130	7	US-10-995-561-13233	A	Sequence 13233, A							
C	164	37.6	1.3	207908	7	US-11-112-908-21	App	Sequence 21, App							
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C	167	37.4	1.3	2784	6	US-10-750-185-56480	A	Sequence 56480, A							
C	168	37.4	1.3	4974	7	US-11-094-586-17	App	Sequence 17, App							
C	169	37.4	1.3	8747	6	US-10-955-054A-141	App	Sequence 141, App							

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 15:39:17 : Search time 2349.36 Seconds
(without alignment)
10464.498 Million cell updates/sec

Title: US-10-073-123-3
Perfect score: 2973
Sequence: 1 ctgctctgctgctcgcc.....tgaaaaaaaaaaaaaaaaa 2973

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database : Published Applications NA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2973	100.0	2973	5	US-10-073-123-3
2	2973	100.0	2973	9	US-10-840-060-134
3	2946	99.1	2961	6	US-10-334-143-134
4	1818	61.2	1818	5	US-10-073-123-1
5	1395.2	46.9	1400	10	US-11-060-756-643
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ALIGNMENTS

RESULT 1

US-09-949-016-2226
; Sequence 2226, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2226
; LENGTH: 2961
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2226

Query Match

Best Local Similarity 99.1%; Score 2946; DB 3; Length 2961;
Matches 2957; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Oy

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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

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9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 101	435.8	14.7	442	1	AI458041	tj66g06.x	AI458041	tj66g06.x	174	312	10.5	765	5	BUI15028	603130876
C 102	433.2	14.6	651	7	CK839519	UI-R-BJ1-	CK839519	UI-R-BJ1-	175	311.8	10.5	431	4	AK187243	Mus muscu
C 103	429.2	14.4	812	3	BI651361	603298288	BI651361	603298288	176	310.6	10.4	610	6	CD535550	LeuKON5.6
C 104	429	14.4	1955	4	AK029910	Mus muscu	AK029910	Mus muscu	177	306	10.3	385	5	BY295911	BY295911
C 105	422.8	14.2	457	1	AU280469	AU280469	AU280469	AU280469	178	305	10.3	732	5	BUI75100	603812175
C 106	422.4	14.2	451	8	N33955	YV26e10.s1	N33955	YV26e10.s1	179	298.4	10.0	396	1	AI020281	AI020281
C 107	421.2	14.2	522	3	BI539241	451495.MA	BI539241	451495.MA	180	296	10.0	619	7	CO786028	BL285A.H1
C 108	417.6	14.0	731	3	BI546406	603188704	BI546406	603188704	181	293	9.9	357	4	AK181083	Mus muscu
C 109	417.6	14.0	781	3	BI586806	603313958	BI586806	603313958	182	291.8	9.8	745	5	BU457443	603772584
C 110	417.2	14.0	761	10	AG179422	Pan trogl	AG179422	Pan trogl	183	291	9.8	745	5	BU312040	BU312040
C 111	413.2	13.9	600	3	BI991408	4094-63.M	BI991408	4094-63.M	184	290	9.8	466	1	AA385793	AA385793
C 112	407	13.7	419	1	AI932977	wo55H08.x	AI932977	wo55H08.x	185	288.4	9.7	829	5	BU211059	BU211059
C 113	404.4	13.6	797	5	BU388136	603859649	BU388136	603859649	186	284.6	9.6	363	1	AJ694597	AJ694597
C 114	401	13.5	402	1	AI061345	an36g09.x	AI061345	an36g09.x	187	284.4	9.6	634	1	AL729451	AL729451
C 115	399	13.4	399	7	CNA11962	170005312	CNA11962	170005312	188	284.2	9.5	664	1	AL729975	AL729975
C 116	397	13.4	397	1	AA412202	2c57a08.r	AA412202	2c57a08.r	189	283.2	9.5	658	1	AL729396	AL729396
C 117	395.6	13.3	3165	4	AK051509	Mus muscu	AK051509	Mus muscu	190	281.6	9.5	914	5	BU911792	AGENCOURT
C 118	395.2	13.3	618	2	BB656726	BB656726	BB656726	BB656726	191	281	9.5	284	1	AA310681	AA310681
C 119	391.6	13.2	618	2	BB655030	BB655030	BB655030	BB655030	192	277.8	9.3	452	1	AA116254	mg06e11.r
C 120	391	13.2	597	3	BI462848	603207827	BI462848	603207827	193	276	9.3	890	5	BU907104	AGENCOURT
C 121	389.4	13.1	831	5	BU229504	603796318	BU229504	603796318	194	271	9.1	738	2	BG076151	BG076151
C 122	388.8	13.1	428	2	BE833910	RC5-OT007	BE833910	RC5-OT007	195	268.8	9.0	540	7	CK977151	4108276.B
C 123	386.8	13.0	446	6	CB545317	AMGNNUC.N	CB545317	AMGNNUC.N	196	267.2	9.0	769	7	CV483699	AGENCOURT
C 124	386	13.0	539	3	BQ329464	MR2-EN009	BQ329464	MR2-EN009	197	265.2	8.9	421	7	CK346041	L0800B09
C 125	383.6	12.9	1205	6	AK050831	Mus muscu	AK050831	Mus muscu	198	265.2	8.9	442	6	CB427346	CB427346
C 126	382.6	12.9	760	6	CA465836	AGENCOURT	CA465836	AGENCOURT	199	265.2	8.9	921	5	BU906849	AGENCOURT
C 127	382.4	12.9	472	1	AA188872	2p77e11.r	AA188872	2p77e11.r	200	264.2	8.9	694	3	BQ193242	UI-R-DR1-
C 128	382.2	12.9	491	2	BG088678	H3156C03-	BG088678	H3156C03-							
C 129	382.2	12.9	714	3	BI650161	603296251	BI650161	603296251							
C 130	379.6	12.8	752	3	BP704585	BP704585	BP704585	BP704585							
C 131	378.4	12.7	719	8	DR719262	AGENCOURT	DR719262	AGENCOURT							
C 132	378.2	12.7	2497	4	AK053727	Mus muscu	AK053727	Mus muscu							
C 133	376.4	12.7	422	1	AA188814	2p77e11.s	AA188814	2p77e11.s							
C 134	376	12.6	376	3	AI275159	QM08b04.x	AI275159	QM08b04.x							
C 135	375	12.6	432	2	CO948790	UMC-p8mm4	CO948790	UMC-p8mm4							
C 136	375	12.6	688	2	BB665419	BB665419	BB665419	BB665419							
C 137	373.6	12.6	633	1	AL855988	AL855988	AL855988	AL855988							
C 138	370	12.4	508	2	BI295519	UI-R-DK0-	BI295519	UI-R-DK0-							
C 139	366.4	12.3	563	8	DN508138	HL0200070	DN508138	HL0200070							
C 140	365	12.3	410	1	AA610160	HP08F08.S	AA610160	HP08F08.S							
C 141	364.6	12.3	543	2	BI110467	602896439	BI110467	602896439							
C 142	364.4	12.3	640	1	AL880653	AL880653	AL880653	AL880653							
C 143	359.8	12.1	697	1	AV717872	AV717872	AV717872	AV717872							
C 144	354.4	11.9	412	1	AA122624	mn33f01.r	AA122624	mn33f01.r							
C 145	350.2	11.8	455	2	BB847775	BB847775	BB847775	BB847775							
C 146	348.4	11.7	666	7	CK959883	4100517.B	CK959883	4100517.B							
C 147	345.6	11.6	753	10	AG520850	Mus muscu	AG520850	Mus muscu							
C 148	345.2	11.6	729	1	AJ657690	AJ657690	AJ657690	AJ657690							
C 149	341.2	11.5	515	2	BE109971	UI-R-BJ1-	BE109971	UI-R-BJ1-							
C 150	340.4	11.4	500	3	BI991619	4103-24.M	BI991619	4103-24.M							
C 151	339	11.4	484	2	BG181388	RST228.At	BG181388	RST228.At							
C 152	338.8	11.4	440	2	BB847793	BB847793	BB847793	BB847793							
C 153	337.8	11.4	748	7	CK237744	AGENCOURT	CK237744	AGENCOURT							
C 154	336.8	11.3	868	6	CB845030	M2PN-0596	CB845030	M2PN-0596							
C 155	336.2	11.3	435	1	AA608209	vm89b06.r	AA608209	vm89b06.r							
C 156	336.2	11.3	648	1	AL879406	AL879406	AL879406	AL879406							
C 157	330	11.1	354	1	AI678492	tu83a11.x	AI678492	tu83a11.x							
C 158	329.8	11.1	378	3	BM150404	TCBAP1D08	BM150404	TCBAP1D08							
C 159	327.8	11.0	522	5	BX527529	BX527529	BX527529	BX527529							
C 160	325.8	11.0	903	5	BUI10146	603127635	BUI10146	603127635							
C 161	322.8	10.9	426	1	AA097213	mk09H04.r	AA097213	mk09H04.r							
C 162	322.6	10.9	432	2	BP556390	UI-R-AL-e	BP556390	UI-R-AL-e							
C 163	320.4	10.8	447	7	BE927292	RC1-CT028	BE927292	RC1-CT028							
C 164	320.2	10.8	887	5	BU217243	603105944	BU217243	603105944							
C 165	319.2	10.7	833	5	BU746851	CH34007.D	BU746851	CH34007.D							
C 166	318.4	10.7	368	1	AA3966939	mr4td11.r	AA3966939	mr4td11.r							
C 167	317	10.7	334	1	AA722551	2980H07.S	AA722551	2980H07.S							
C 168	316.8	10.7	521	1	AA124664	mp79e07.r	AA124664	mp79e07.r							

ALIGNMENTS

RESULT 1	CR618625	2927 bp	mRNA	linear	HTC 21-JUL-2004
LOCUS	CR618625	full-length cDNA clone	CS0DF030Y121	of fetal brain of Homo sapiens	
DEFINITION	CR618625	full-length cDNA clone	CS0DF030Y121	of fetal brain of Homo sapiens	
ACCESSION	CR618625.1	GI:50499432			
VERSION	CR618625.1	HTC; CDS; CDS			
KEYWORDS	HTC; CDS; CDS				
SOURCE	CR618625	HTC; CDS; CDS			
ORGANISM	CR618625	HTC; CDS; CDS			
REFERENCE	CR618625	HTC; CDS; CDS			
AUTHORS	CR618625	HTC; CDS; CDS			
TITLE	CR618625	HTC; CDS; CDS			
JOURNAL	CR618625	HTC; CDS; CDS			
REMARK	CR618625	HTC; CDS; CDS			
REFERENCE	CR618625	HTC; CDS; CDS			
AUTHORS	CR618625	HTC; CDS; CDS			
TITLE	CR618625	HTC; CDS; CDS			
JOURNAL	CR618625	HTC; CDS; CDS			
COMMENT	CR618625	HTC; CDS; CDS			
FEATURES	CR618625	HTC; CDS; CDS			
SOURCE	CR618625	HTC; CDS; CDS			

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 15:22:00 ; Search time 1735.03 Seconds
(without alignments)
11420.080 Million cell updates/sec

Title: US-10-073-123-3
Perfect score: 2973
Sequence: 1 ctggctgtgtcgtcgcgc.....tgaaaaaaaaaaaaaaaaa 2973

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database : N Geneseq_21.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001s.*

5: Geneseqn2001bs.*

6: Geneseqn2002s.*

7: Geneseqn2002bs.*

8: Geneseqn2003s.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004s.*

13: Geneseqn2004bs.*

14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2973	100.0	2973	6	AB552510 Human amp
2	2973	100.0	2973	10	ADK11345 Human Wip
3	2946	99.1	2961	10	ADK41027 Novel hum
4	2946	99.1	2961	13	ADK15741 Kinase 60
5	1472	49.5	1719	4	AAK91530 Human dig
6	448	15.1	996	6	ABQ45100 Oligonuc
7	448	15.1	996	6	ABQ45101 Oligonuc
8	430.8	14.5	996	6	ABQ45098 Oligonuc
9	430.8	14.5	996	6	ABQ45099 Oligonuc
10	370.8	12.5	478	10	ADD35192 Mouse mit
11	319	10.7	366	13	ADU09876 Solid tum
12	292	9.8	292	10	ADK11965 Breast ca
13	292	9.8	292	14	ADK11965 Human col
14	268	9.0	735	10	ADD35191 Mouse mit
15	246.8	8.3	631	10	ADK11602 Toxicity
16	171	5.8	4901	4	ABL05477 Drosophil
17	171	5.8	4901	10	ADK11343 Drosophil
18	99.2	3.3	8256	4	ABL05476 Drosophil
19	90.4	3.0	357	8	ABX49504 Bovine ES

c	20	68.2	2.3	8056	8	ABZ10246	Abz10246 Haematopo
	21	68	2.3	119	12	ADL86309	Adl86309 DNA up-re
	22	68	2.3	119	12	ADL86308	Adl86308 DNA up-re
c	23	66.6	2.2	8056	8	ABZ10100	Abz10100 Haematopo
	24	65.8	2.2	18624	6	ABL33702	Ab133702 Human imm
	25	64.4	2.2	5006	5	AAD22381	Aad22381 Cotton ol
	26	62	2.1	62	13	ADR00046	Adr00046 PPMID PCR
c	27	61.8	2.1	16217	6	ABL32624	Ab132624 Human imm
	28	60	2.0	60	6	ABN58833	Abn58833 Human spl
	29	60	2.0	60	6	ABN58576	Abn58576 Human spl
	30	60	2.0	60	6	ABN38820	Abn38820 Human spl
	31	60	2.0	60	6	ABN58577	Abn58577 Human spl
	32	60	2.0	60	6	ABN58578	Abn58578 Human spl
	33	60	2.0	2000	11	ACL35887	ACL35887 Rice stre
c	34	60	2.0	110000	13	ABD32968_6	Continuation (7 of
	35	59.8	2.0	8093	4	AAS46435	Aas46435 Tumour su
	36	59.8	2.0	8093	6	ABK33973	Abk33973 Human DNA
	37	59.8	2.0	8093	6	ABL92236	Ab192236 Chemical
	38	59.8	2.0	8093	6	ABL49331	Ab149331 Human MLH
	39	59.8	2.0	8093	8	ABZ10031	Abz10031 Haematopo
	40	59.8	2.0	8093	8	ADA20360	Ada20360 Prostate
	41	59.8	2.0	8093	8	ADA84167	Ada84167 Human ren
	42	59.8	2.0	8093	10	ADB54139	Adb54139 Pretreate
	43	59.8	2.0	8093	10	ADE84113	Ad84113 Human lym
	44	59.8	2.0	8093	13	ADS89291	Ad89291 Oligonuc
	45	59.8	2.0	17213	6	ABL33482	Ab133482 Human imm
	46	59.6	2.0	2000	11	ACL37108	ACL37108 Rice stre
c	47	59.4	2.0	8170	6	ABK28257	Abk28257 DNA trans
c	48	59.2	2.0	2000	11	ACL35887	ACL35887 Rice stre
	49	58.8	2.0	954	14	ADZ71043	Adz71043 Human chr
	50	58.8	2.0	8093	8	ABZ10177	Abz10177 Haematopo
	51	58.8	2.0	8093	10	ADB54267	Adb54267 Pretreate
	52	58.8	2.0	8093	10	ADE84189	Ad84189 Human lym
	53	58.8	2.0	8093	13	ADS89565	Ad89565 Oligonuc
	54	58.6	2.0	17967	6	ABL33015	Ab133015 Human imm
c	55	58.4	2.0	2000	11	ACL35363	ACL35363 Rice stre
	56	58	2.0	37973	6	ABL34197	Ab134197 Human imm
	57	57.6	1.9	2000	8	ADA71938	Ada71938 Rice gene
	58	57.6	1.9	15373	6	ABL32467	Ab132467 Human imm
c	59	57.2	1.9	6816	12	ADQ24856	Adq24856 Human sof
	60	57.2	1.9	8056	8	ABZ10100	Abz10100 Haematopo
	61	57.2	1.9	17869	6	ABK39920	Abk39920 Human chr
	62	57.2	1.9	17869	6	ABL32104	Ab132104 Human imm
	63	56.6	1.9	1162	14	ADZ71022	Adz71022 Human chr
	64	56.6	1.9	8170	6	ABK28258	Abk28258 DNA trans
	65	56.4	1.9	883	4	AAL15210	Aal15210 Human bre
c	66	56.4	1.9	960	11	ACN85231	Acn85231 Breast ca
	67	56.2	1.9	2000	8	ADA71938	Ada71938 Rice gene
c	68	55.4	1.9	2000	11	ACL35363	ACL35363 Rice stre
	69	55.4	1.9	3315	14	ADM71859	Adm71859 OKT3Vb an
c	70	55.4	1.9	5875	6	ABL32289	Ab132289 Human imm
	71	55.4	1.9	8056	8	ABZ10246	Abz10246 Haematopo
	72	55.2	1.9	6121	6	ABL34478	Ab134478 Human met
	73	55.2	1.9	6121	6	ABL70151	Ab170151 Chemical
	74	55.2	1.9	6121	7	ADS99739	Ad99739 Bisulphit
	75	55.2	1.9	6121	7	ADS99739	Ad99739 Bisulphit
	76	55	1.8	9155	6	ABL32462	Ab132462 Human imm
	77	54.8	1.8	6061	6	ABL32141	Ab132141 Human imm
	78	54.8	1.8	6308	6	ABL33470	Ab133470 Human imm
	79	54.8	1.8	50000	6	ABL55644	Ab155644 AmEPV gen
c	80	54.8	1.8	110000	3	AAF22305_05	Continuation (6 of
	81	54.6	1.8	5376	6	ABL34150	Ab134150 Human imm
	82	54.4	1.8	8067	6	ABN80224	Abn80224 Human che
	83	54.2	1.8	15355	13	ADS89399	Ad89399 Oligonuc
	84	54.2	1.8	15355	13	ADS89673	Ad89673 Oligonuc
	85	54.2	1.8	16602	6	ABL32726	Ab132726 Human imm
	86	54.2	1.8	16602	6	ABN80068	Abn80068 Human che
	87	54.2	1.8	18357	6	ABQ67083	Abq67083 Human ang
	88	54	1.8	3287	8	ABZ10192	Abz10192 Haematopo
c	89	54	1.8	7340	6	AAD28379	Aad28379 Human che
	90	53.2	1.8	1554	14	ADZ70999	Adz70999 Human chr
	91	53.2	1.8	19459	6	ABK31213	Abk31213 Signal tr
	92	53.2	1.8	19459	6	ABL70528	Ab170528 Chemical

C	93	53	1.8	1554	14	ADZ70999	Adz70999 Human chr
	94	53	1.8	6092	6	AAS61079	Aas61079 Human gen
	95	52.8	1.8	6106	4	AAS46429	Aas46429 Tumour su
	96	52.8	1.8	6106	6	ABK40031	Abk40031 Human che
	97	52.8	1.8	6106	6	ABL33472	AbL33472 Human imm
	98	52.8	1.8	9502	4	AAS46731	Aas46731 Tumour su
	99	52.8	1.8	11790	6	ABL32542	AbL32542 Human imm
	100	52.8	1.8	14307	6	ABL32728	AbL32728 Human imm
	101	52.6	1.8	2974	2	AAQ79630	Aaq79630 Partial P
	102	52.6	1.8	5696	6	ABL33106	AbL33106 Human imm
	103	52.6	1.8	5696	6	ABK31288	AbK31288 Signal tr
	104	52.6	1.8	9524	6	ABK39993	AbK39993 Human che
	105	52.6	1.8	9524	6	ABL32838	AbL32838 Human imm
	106	52.6	1.8	34548	6	ABL70603	AbL70603 Chemicall
	107	52.4	1.8	5807	6	ABL33155	AbL33155 Human imm
	108	52.4	1.8	11805	6	ABL33749	AbL33749 Human che
	109	52.2	1.8	6175	6	RAD28373	Rad28373 Human che
	110	52.2	1.8	8964	6	ABL33535	AbL33535 Human imm
	111	52.2	1.8	8964	6	ABK31373	AbK31373 Signal tr
	112	52.2	1.8	8964	6	ABL70582	AbL70582 Chemicall
	113	52.2	1.8	8964	6	AAS61277	Aas61277 Human gen
	114	52.2	1.8	110000	5	AAI61373_0	Aai61373 Soybean 3
	115	52.2	1.8	110000	5	AAI61373_1	Continuation (2 of
	116	52.2	1.8	158001	12	ADL17884	Adl17884 Human pho
	117	52	1.7	6167	6	ABK28370	AbK28370 DNA trans
	118	51.8	1.7	1428	14	ADZ70899	Adz70899 Human mat
	119	51.8	1.7	6024	6	ABL33647	AbL33647 Human imm
	120	51.8	1.7	7047	6	ABK28385	AbK28385 DNA trans
	121	51.8	1.7	16439	6	ABL32887	AbL32887 Human imm
	122	51.8	1.7	19653	6	ABL33334	AbL33334 Human imm
	123	51.6	1.7	3315	14	ADW17859	Adw17859 OKT3Vb an
	124	51.6	1.7	6866	6	ABL32667	AbL32667 Human imm
	125	51.6	1.7	6866	6	ABL49320	AbL49320 Human pol
	126	51.6	1.7	7346	6	ABL32345	AbL32345 Human imm
	127	51.6	1.7	7667	4	AAS46333	Aas46333 Tumour su
	128	51.6	1.7	19659	6	ABL32767	AbL32767 Human imm
	129	51.4	1.7	2000	11	ACL37108	AcL37108 Rice stre
	130	51.4	1.7	11422	6	ABK39936	AbK39936 Human che
	131	51.4	1.7	11422	6	ABL32218	AbL32218 Human imm
	132	51.4	1.7	18512	6	ABL32976	AbL32976 Human imm
	133	51.4	1.7	94911	12	ADQ97846	Adq97846 Human can
	134	51.2	1.7	5001	6	ABK33950	AbK33950 Human DNA
	135	51.2	1.7	5001	6	ABL54373	AbL54373 Chemicall
	136	51.2	1.7	5001	8	ADA20404	Ada20404 Prostata
	137	51.2	1.7	5001	8	ADA84211	Ada84211 Human ren
	138	51.2	1.7	15738	10	ADI23932	Adi23932 Streptomy
	139	51.2	1.7	16579	10	ADB54245	AdB54245 Pretreate
	140	51.2	1.7	16579	10	ADE37772	Ade37772 Human che
	141	51.2	1.7	16579	13	ADS89547	Ads89547 Oligonuc1
	142	51.2	1.7	34688	6	ABQ67060	AbQ67060 Human ang
	143	51.2	1.7	61944	10	ADI23920	Adi23920 Streptomy
	144	51.2	1.7	114955	2	AXS3491	Axs3491 Human ade
	145	51	1.7	4661	6	ABQ67022	AbQ67022 Human ang
	146	51	1.7	5360	6	ABL33936	AbL33936 Human imm
	147	51	1.7	5360	6	ABL92296	AbL92296 Chemicall
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ALIGNMENTS

RESULT 1

ABSS2510

ID ABS2510 standard; cDNA; 2973 BP.

XX AC ABS2510;

XX DT 15-NOV-2002 (first entry)

XX DE Human amplified cancer gene, WIPI, cDNA.

XX KW Human; gene; ss; WIPI; cancer; cytostatic; diagnosis; gene copy number;

XX KW precancerous; cancerous; precancerous lesion; gene therapy;

XX KW gene function; therapeutic; tumour; chromosome 17q23; stress inducible;

XX KW p53; protein phosphatase type 2C; PP2C.

XX OS Homo sapiens.

XX EH Key Location/Qualifiers

XX FT CDS 204..2021

XX FT /*tag= a

XX FT /product= "WIPI"

XX FT /note= "This CDS is specifically claimed in claim 25"

XX PN WO200264838-A2.

XX PD 22-AUG-2002.

XX PD 12-FEB-2002; 2002WO-US003991.

XX PD 14-FEB-2001; 2001US-0268362P.

XX PD (TULA-) TULARIK INC.

XX XX

GenCore version 5.1.6
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c 102	61.8	2.1	343050	2	PFAP29353	Plasmodiu	AL929353	Plasmodiu	c 175	58.4	2.0	106763	8	AP002091		Continuation (6 of
c 103	61.2	2.1	195072	14	AX908786	Danio rer	AX908786	Danio rer	c 176	58.4	2.0	110000	14	PFMAL8P1_05		AP000920 Homo sapi
104	61.2	2.1	241173	14	AC126150	Rattus no	AC126150	Rattus no	c 177	58.4	2.0	114349	8	AP000920		AC004061 Homo sapi
c 105	61	2.1	85779	15	SCE011856		SCE011856		c 178	58.4	2.0	117101	8	AC004061		AC149953 Strongylo
c 106	61	2.1	155048	14	CR450727	Danio rer	CR450727	Danio rer	c 179	58.4	2.0	141721	14	AC149953		CR152229 Danio rer
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c 109	60.4	2.0	197142	14	CR388410	Danio rer	CR388410	Danio rer	c 182	58.4	2.0	191041	8	AC091742		AC083952 Homo sapi
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AUTHORS		REFERENCE		Sequence 3 from Patent WO02064838.	2973 bp	DNA	linear	PAT 22-MAR-2003
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; APPLICANT: DeNISE, Sue K.													
; APPLICANT: KERR, Richard													
; APPLICANT: ROSENFELD, David													
; APPLICANT: HOLM, Tom													
; APPLICANT: BATES, Stephen													
; APPLICANT: FANTIN, Dennis													
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; CURRENT FILING DATE: 2003-12-31													
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	316.8	17.4	996	8	US-10-363-345A-31689
8	316.8	17.4	996	8	US-10-363-345A-31690
9	316.8	17.4	996	9	US-10-363-483A-31689
10	316.8	17.4	996	9	US-10-363-483A-31690
11	301	16.6	996	8	US-10-363-345A-31691
12	301	16.6	996	8	US-10-363-345A-31692
13	301	16.6	996	9	US-10-363-483A-31691
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6	15738	6	6	US-10-329-079-46	Sequence 46, Appl
6	61944	6	6	US-10-329-079-34	Sequence 34, Appl
6	32329	6	6	US-10-374-903A-1	Sequence 1, Appl
7	1862	7	7	US-10-767-701-12741	Sequence 12741, A
8	493	8	8	US-10-425-115-72990	Sequence 72990, A
7	1339	7	7	US-10-437-963-10842	Sequence 10842, A
7	2891	7	7	US-10-437-963-2500	Sequence 2500, Ap
6	629	6	6	US-10-437-963-48494	Sequence 48494, A
7	1304	7	7	US-10-437-963-19773	Sequence 19773, A
9	444	9	9	US-10-857-294-394	Sequence 394, App
7	630	7	7	US-10-437-963-11527	Sequence 11527, A
6	1375	6	6	US-10-437-963-11531	Sequence 11531, A
8	889	8	8	US-10-739-930-4553	Sequence 4553, Ap
7	2535	7	7	US-10-479-435-38	Sequence 38, Appl
9	15624	9	9	US-10-760-493-30	Sequence 30, Appl
9	164051	9	9	US-10-760-493-18	Sequence 18, Appl
7	549	7	7	US-10-437-963-11526	Sequence 11526, A
7	813	7	7	US-10-437-963-19780	Sequence 19780, A
7	1287	7	7	US-10-260-238-845	Sequence 845, App
8	972	8	8	US-10-425-115-17653	Sequence 17653, A
3	688	3	3	US-09-981-876-73	Sequence 73, Appl
3	688	3	3	US-09-148-545-73	Sequence 73, Appl
9	688	9	9	US-10-979-111-73	Sequence 73, Appl
6	24081	6	6	US-10-132-134-13	Sequence 13, Appl
6	52101	6	6	US-10-132-134-1	Sequence 1, Appl
7	987	7	7	US-10-374-780A-580	Sequence 580, App
7	987	7	7	US-10-412-699B-1077	Sequence 1077, Ap
7	321	7	7	US-10-182-327-163	Sequence 163, App
7	462	7	7	US-10-437-963-77570	Sequence 77570, A
7	498	7	7	US-10-767-701-1917	Sequence 1917, Ap
6	1755	6	6	US-10-369-493-40542	Sequence 40542, A
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7	1167	7	7	US-10-437-963-63792	Sequence 63792, A
7	3459	7	7	US-10-311-795-3	Sequence 3, Appl
9	3459	9	9	US-10-756-149-1720	Sequence 1720, Ap
8	429	8	8	US-10-425-115-29133	Sequence 29133, A
7	468	7	7	US-10-282-122A-25614	Sequence 25614, A
5	540	5	5	US-10-437-963-32260	Sequence 32260, A
7	777	7	7	US-10-029-386-20524	Sequence 20524, A
9	5208	9	9	US-10-937-379-42	Sequence 42, Appl
6	7359	6	6	US-10-937-379-24	Sequence 24, Appl
6	728	6	6	US-10-029-386-24125	Sequence 24125, A
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6	6706	6	6	US-10-756-149-3015	Sequence 3015, Ap
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4	1427	4	4	US-10-659-868-25	Sequence 25, Appl
3	1813	3	3	US-09-880-578-3	Sequence 3, Appl
3	2079	3	3	US-09-037-657-43	Sequence 43, Appl
7	357	7	7	US-09-960-352-14669	Sequence 14669, A
4	1632	4	4	US-10-437-963-52545	Sequence 52545, A
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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65	41.4	2.3	7808	3	US-08-949-386-22	Sequence 22, Appl
66	41.4	2.3	7808	3	US-08-450-562-22	Sequence 22, Appl
67	41.4	2.3	7808	3	US-08-984-709A-22	Sequence 22, Appl
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72	41.2	2.3	927	3	US-09-107-433-432	Sequence 432, App
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80	41.2	2.3	2561	3	US-09-976-740-48	Sequence 48, Appl
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83	41	2.3	18079	3	US-09-949-016-13344	Sequence 13344, A
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c 110	40.4	2.2	6721	3	US-09-949-016-518	Sequence 518, App	Sequence 518, App	Sequence 103, App
c 111	40.4	2.2	15644	3	US-09-902-540-1133	Sequence 1133, Ap	Sequence 1133, Ap	Sequence 13, Appl
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c 137	39.6	2.2	2003	2	US-08-469-526A-21	Sequence 21, Appl	Sequence 21, Appl	Sequence 1, Appli
c 138	39.6	2.2	2003	2	US-08-734-591A-21	Sequence 21, Appl	Sequence 21, Appl	Sequence 1, Appli
c 139	39.6	2.2	2003	3	US-08-341-018-71	Sequence 71, Appl	Sequence 71, Appl	Sequence 1, Appli
c 140	39.6	2.2	2003	3	US-08-470-335-21	Sequence 21, Appl	Sequence 21, Appl	Sequence 1, Appli
c 141	39.6	2.2	2003	3	US-08-735-021-21	Sequence 21, Appl	Sequence 21, Appl	Sequence 1, Appli
c 142	39.6	2.2	2003	3	US-08-734-664A-21	Sequence 21, Appl	Sequence 21, Appl	Sequence 1, Appli
c 143	39.6	2.2	2003	3	US-08-470-339-21	Sequence 21, Appl	Sequence 21, Appl	Sequence 1, Appli
c 144	39.6	2.2	2003	3	US-08-467-602-21	Sequence 21, Appl	Sequence 21, Appl	Sequence 1, Appli
c 145	39.6	2.2	3538	3	US-09-902-540-528	Sequence 528, App	Sequence 528, App	Sequence 1, Appli
c 146	39.6	2.2	4308	3	US-09-999-833A-527	Sequence 527, App	Sequence 527, App	Sequence 1, Appli
c 147	39.6	2.2	4308	3	US-10-020-445A-527	Sequence 527, App	Sequence 527, App	Sequence 1, Appli
c 148	39.6	2.2	18471	3	US-09-902-540-1167	Sequence 1167, Ap	Sequence 1167, Ap	Sequence 1, Appli
c 149	39.6	2.2	37875	3	US-09-949-016-13182	Sequence 13182, A	Sequence 13182, A	Sequence 1, Appli
c 150	39.6	2.2	58857	3	US-09-477-962-1	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli
c 151	39.6	2.2	222691	3	US-09-949-016-11762	Sequence 11762, A	Sequence 11762, A	Sequence 1, Appli
c 152	39.6	2.2	222697	3	US-09-949-016-15842	Sequence 15842, A	Sequence 15842, A	Sequence 1, Appli
c 153	39.4	2.2	601	3	US-09-949-016-48721	Sequence 48721, A	Sequence 48721, A	Sequence 1, Appli
c 154	39.4	2.2	2065	3	US-08-335-865J-8	Sequence 8, Appli	Sequence 8, Appli	Sequence 1, Appli
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c 156	39.4	2.2	2923	2	US-08-377-292-6	Sequence 6, Appli	Sequence 6, Appli	Sequence 1, Appli
c 157	39.4	2.2	2923	2	US-07-989-847-7	Sequence 7, Appli	Sequence 7, Appli	Sequence 1, Appli
c 158	39.4	2.2	2923	3	US-08-469-411-7	Sequence 7, Appli	Sequence 7, Appli	Sequence 1, Appli
c 159	39.4	2.2	2923	3	US-09-780-601A-7	Sequence 7, Appli	Sequence 7, Appli	Sequence 1, Appli
c 160	39.4	2.2	2943	3	US-09-949-016-247	Sequence 247, App	Sequence 247, App	Sequence 1, Appli
c 161	39.4	2.2	33152	3	US-09-949-016-16719	Sequence 16719, A	Sequence 16719, A	Sequence 1, Appli
c 162	39.4	2.2	158735	3	US-09-949-016-11989	Sequence 11989, A	Sequence 11989, A	Sequence 1, Appli
c 163	39.4	2.2	158735	3	US-09-949-016-17130	Sequence 17130, A	Sequence 17130, A	Sequence 1, Appli
c 164	39.2	2.2	985	3	US-09-056-556-182	Sequence 182, App	Sequence 182, App	Sequence 1, Appli
c 165	39.2	2.2	985	3	US-09-072-596-177	Sequence 177, App	Sequence 177, App	Sequence 1, Appli
c 166	39.2	2.2	985	3	US-09-072-967-182	Sequence 182, App	Sequence 182, App	Sequence 1, Appli
c 167	39.2	2.2	985	3	US-10-193-002-177	Sequence 177, App	Sequence 177, App	Sequence 1, Appli
c 168	39.2	2.2	985	3	US-10-084-843-182	Sequence 182, App	Sequence 182, App	Sequence 1, Appli
c 169	39.2	2.2	1018	2	US-08-444-083-7	Sequence 7, Appli	Sequence 7, Appli	Sequence 1, Appli
c 170	39.2	2.2	1018	2	US-08-286-304-7	Sequence 7, Appli	Sequence 7, Appli	Sequence 1, Appli

96	318.4	17.5	368	1	AA396939	mr41d11.r	AA396939	169	219.8	12.1	864	7	CJ375970	CJ375970
97	316.6	17.4	316	8	DT110018	JGI_ANNO6	DT110018	170	217.2	11.9	442	6	CB427346	602917 MA
98	314.8	17.3	357	2	BF995912	RCS-GN019	BF995912	171	216.2	11.9	528	6	CB273832	mai85c04.
99	312	17.2	353	2	BF515693	UI-H-BW1	BF515693	172	216.2	11.9	846	7	CK796994	AGENCOURT
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101	311.8	17.2	431	4	AK187243	Mus muscu	AK187243	174	212.8	11.7	747	7	CK694781	2f101-P00
102	306	16.8	385	5	BY295911	BY295911	BY295911	175	210.6	11.6	511	1	AW639011	bl177e05.w
103	305	16.8	732	5	BUI375100	G03812175	BUI375100	176	209	11.5	890	6	CA790116	AGENCOURT
104	300.2	16.5	488	2	BGI01153	uy20a08.Y	BGI01153	177	208.8	11.5	813	9	CC570133	CH240_445
105	300	16.5	753	10	AG520850	Mus muscu	AG520850	178	208	11.4	800	9	B2274588	CH230-355
106	298.4	16.4	396	1	A1020281	ub16b02.r	A1020281	179	204.6	11.3	915	6	CD778547	B274588
107	298.4	16.4	618	2	BB655030	BB655030	BB655030	180	203.8	11.2	619	6	CA378435	EST49908
108	298.4	16.4	2497	4	AK053727	Mus muscu	AK053727	181	203.4	11.2	455	7	CK614315	657313 NC
109	298.4	16.4	3165	4	AK051509	Mus muscu	AK051509	182	201.6	11.1	444	5	BY382594	LPSe GL15
110	298	16.4	615	2	BB656726	BB656726	BB656726	183	201.6	11.1	838	7	CR564245	BY382594
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112	296	16.3	1955	4	AK029910	Mus muscu	AK029910	185	199.2	11.0	761	2	CN327806	AGENCOURT
113	295.2	16.2	688	2	BB665419	BB665419	BB665419	186	199	10.9	666	5	BI079680	602874630
114	293	16.1	357	4	AK181083	Mus muscu	AK181083	187	198.6	10.9	644	3	BW732636	BW732636
115	292	16.1	709	6	CD365828	UI-H-FT2-	CD365828	188	197.6	10.9	447	2	BE927292	RC1-CT028
116	292	16.1	711	6	CD367090	UI-H-FT2-	CD367090	189	197	10.8	825	6	CF253530	mdv104 h
117	291	16.0	745	5	BUI312040	G03544376	BUI312040	190	195.8	10.8	375	2	BG100789	uy14h01.Y
118	290.8	16.0	709	6	CA314288	UI-CF-FE0	CA314288	191	195.2	10.7	563	8	DN508138	HL0200070
119	287.4	15.8	745	5	BU457443	G03772584	BU457443	192	195	10.7	397	1	AA412202	ZC57a08.r
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121	286.4	15.8	903	5	BUI10146	G03127635	BUI10146	194	193	10.6	294	1	BB045763	BB045763
122	285.6	15.7	515	2	BE108971	UI-R-BJ1-	BE108971	195	190.4	10.5	355	2	BF715165	mab05h12.
123	284.6	15.7	363	1	AJ694597	AJ694597	AJ694597	196	189.2	10.4	811	7	CN843661	AGENCOURT
124	284	15.6	634	1	AL729451	AL729451	AL729451	197	187	10.3	415	2	BB680262	BB680262
125	284.2	15.6	668	1	AL729975	AL729975	AL729975	198	185.6	10.2	714	5	BW259302	BW259302
126	283.2	15.6	654	1	AL729396	AL729396	AL729396	199	185.4	10.2	827	6	CD750838	AGENCOURT
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128	281.6	15.5	914	5	BUI911792	AGENCOURT	BUI911792							
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133	273	15.0	898	8	CX784650	HESC3_37	CX784650							
134	272.2	15.0	714	3	BI650161	G03296251	BI650161							
135	267.2	14.7	769	7	CV483699	AGENCOURT	CV483699							
136	265.2	14.6	921	5	BUI906849	AGENCOURT	BUI906849							
137	262	14.4	829	5	BUI211059	G03102418	BUI211059							
138	261	14.4	964	5	BUI913726	AGENCOURT	BUI913726							
139	259	14.2	887	7	CO919640	AGENCOURT	CO919640							
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141	249.4	13.7	693	7	CK960038	4100901 B	CK960038							
142	247.2	13.6	795	3	BI886556	ZF637-1-0	BI886556							
143	246.4	13.6	378	2	BB737019	BB737019	BB737019							
144	246.2	13.5	799	7	CN177738	AGENCOURT	CN177738							
145	245.8	13.5	350	3	BQ302915	CM1-BT061	BQ302915							
146	245	13.5	415	6	CB800364	AMGNNUC:S	CB800364							
147	244.2	13.4	702	8	DR726939	AGENCOURT	DR726939							
148	244	13.4	285	2	BF910408	PM4-UT003	BF910408							
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152	242.4	13.3	452	1	AW853923	RC3-CT025	AW853923							
153	242.2	13.3	863	7	CN315990	AGENCOURT	CN315990							
154	239.8	13.2	522	5	BX527529	BX527529	BX527529							
155	239.4	13.2	493	6	CD617279	56086835J	CD617279							
156	238.8	13.1	761	5	EX847410	EX847410	EX847410							
157	236.6	13.0	466	1	AA985793	ua66g10.r	AA985793							
158	236.2	13.0	801	6	CB310370	AGENCOURT	CB310370							
159	236	12.9	682	5	BW262305	BW262305	BW262305							
160	233.8	12.9	421	7	CK346041	L0800B09-	CK346041							
161	233.2	12.8	896	7	CK799175	AGENCOURT	CK799175							
162	231.4	12.7	887	7	CK797067	AGENCOURT	CK797067							
163	227.8	12.5	452	1	AA116254	mq06e11.r	AA116254							
164	227.8	12.5	521	1	AA124664	mp79e07.r	AA124664							
165	225.4	12.4	836	1	AM031095	AM031095	AM031095							
166	224.8	12.4	635	2	BB616277	BB616277	BB616277							
167	224	12.3	739	7	CJ354166	CJ354166	CJ354166							
168	219.8	12.1	457	1	AU280469	AU280469	AU280469							

RESULT 1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

DO029466

Homo sapiens PPMD gene, VIRTUAL TRANSCRIPT, partial sequence,

1818 bp

DNA

linear

GSS 02-JUN-2005

DO029466

Genomic survey sequence.

DO029466.1

GI:66880670

GSS.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1818)

Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

A scan for positively selected genes in the genomes of humans and chimpanzees

(er) PLoS Biol. 3 (6), E170 (2005)

15869325

2 (bases 1 to 1818)

Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

Direct Submission

Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

Location/Qualifiers

1..1818

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 15:22:00 ; Search time 1060.97 Seconds
(without alignment)
11420.080 Million cell updates/sec

Title: US-10-073-123-1

Perfect score: 1818

Sequence: 1 atgcgggcgtactgct.....aaactgttctgttctgta 1818

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database :

1: Geneseqn_21.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1818	100.0	2961	10	ADK41027 Novel hum
2	1818	100.0	2961	13	ADR15741 Kinase 60
3	1818	100.0	2973	6	ABS52510 Human amp
4	1818	100.0	2973	10	ADK11345 Human Wip
5	536	29.5	1719	4	AAK91530 Human dig
6	370.8	20.4	478	10	ADD35192 Mouse mit
7	316.8	17.4	996	6	ABQ45098 Oligonucle
8	316.8	17.4	996	6	ABQ45099 Oligonucle
9	301	16.6	996	6	ABQ45100 Oligonucle
10	301	16.6	996	6	ABQ45101 Oligonucle
11	171	9.4	4901	10	ABL05477 Drosophil
12	171	9.4	4901	10	ADK11343 Drosophil
13	99.2	5.5	8256	4	ABL05476 Drosophil
14	62	3.4	62	13	ADRO0046 PCR
15	60	3.3	60	6	ABN58833 Human spl
16	60	3.3	60	6	ABN58576 Human spl
17	60	3.3	60	6	ABN38820 Human spl
18	60	3.3	60	6	ABN58577 Human spl
19	57.6	3.2	2000	8	ADA71938 Rice gene

20	52.6	2.9	2974	2	AAQ79630 Partial P
21	51.2	2.8	15738	10	ADI23332 Streptomy
22	51.2	2.8	61944	10	ADI23320 Streptomy
23	50.8	2.8	32329	12	ADOS1695 Streptomy
24	50.4	2.8	3240	14	ABE91819 DNA encod
C 25	50.4	2.8	110000	4	AAI99682_39
C 26	50.4	2.8	110000	4	AAI99683_39
27	48.2	2.7	13695	3	ABN97984_39
28	47.8	2.6	444	14	ADV90740 Cow milk
C 29	47.6	2.6	114955	2	AA533491 Human ade
C 30	47.2	2.6	889	13	ADT19227 Human nuc
C 31	47.2	2.6	2535	10	AA51682 Human nuc
C 32	47.2	2.6	15624	13	ADQ91707 Polyketid
C 33	47.2	2.6	15624	13	ABE86999 Streptomy
C 34	47.2	2.6	15624	13	ABE86796 Streptomy
C 35	47.2	2.6	164051	13	ADQ91695 Polyketid
C 36	47.2	2.6	164051	13	ABE86862 Streptomy
C 37	47.2	2.6	164051	13	ABE86659 Streptomy
C 38	47	2.6	1287	12	ADJ39845 Plant cDN
C 39	47	2.6	2000	8	ADA71539 Rice gene
40	46.4	2.6	688	2	AAV34216 Human sec
41	46.4	2.6	688	8	ACD08087 cDNA enco
42	46.4	2.6	688	14	ADZ12273 Human sec
43	46.4	2.6	2000	11	ACL36471 Rice stre
C 44	46.2	2.5	24081	10	AA54223 Streptomy
C 45	46.2	2.5	52101	10	AA54217 Streptomy
C 46	46	2.5	987	12	ADI42117 Plant tra
47	46	2.5	987	12	ADO02664 Corn orth
C 48	45.8	2.5	321	5	AAI13973 Human S
C 49	45.8	2.5	700	3	AAA37651 FMR1 gene
C 50	45.8	2.5	1755	13	ADT42104 Bacterial
C 51	45.6	2.5	2160	14	ABE12322 Human HCN
C 52	45.6	2.5	2670	14	ABE12298 Human HCN
C 53	45.6	2.5	3372	13	ADQ83419 Human tum
C 54	45.6	2.5	3431	4	AAH98302 Human EST
C 55	45.6	2.5	3459	6	AAH98302 Human EST
C 56	45.4	2.5	468	8	ACA37744 Prokaryot
57	45.4	2.5	777	12	ACH87329 Human gen
58	45.4	2.5	5208	14	ADY72593 A. orient
C 59	45.4	2.5	7599	11	ADM29297 Human nov
C 60	45.4	2.5	7599	11	ADM29295 Human nov
61	45.4	2.5	73599	14	ADY72575 Polyene p
C 62	45.2	2.5	705	11	ACL29071 Rice abio
63	45.2	2.5	728	12	ACH90930 Human gen
C 64	45.2	2.5	3132	14	ADZ49365 Insulin s
C 65	45.2	2.5	3632	2	AAV61586 Alpha-1A
C 66	45	2.5	2874	8	ACA40307 Prokaryot
C 67	45	2.5	6706	11	ADN95160 Human BEC
68	45	2.5	6706	12	ADQ20401 Human sof
69	45	2.5	6729	12	ADQ24402 Human sof
70	45	2.5	110000	4	AAI99682_03
C 71	44.8	2.5	227968	6	AAH83497 Human cDN
C 72	44.8	2.5	227968	12	ADQ18538 Human sof
73	44.4	2.4	2160	14	ABE12322 Human HCN
74	44.4	2.4	2670	14	ABE12298 Human HCN
75	44.4	2.4	3372	13	ADQ83419 Human tum
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C 78	44.4	2.4	10144	6	ABN95670 Gene #216
79	44.2	2.4	1060	13	ADX31432 Plant ful
80	44.2	2.4	1749	11	ACL29333 Rice abio
81	44.2	2.4	114955	2	AA533491 Human ade
C 82	44	2.4	966	14	AEA26884 Stress to
C 83	44	2.4	1427	8	ACD07381 Rice Myb-
C 84	44	2.4	1427	12	ADJ77726 cDNA enco
85	44	2.4	1813	2	AAV70895 cDNA enco
86	44	2.4	2079	4	AAQ04199 Murine ha
C 87	44	2.4	2562	14	ABE91823 DNA encod
C 88	44	2.4	3453	14	ACL68250 M. xanthu
C 89	44	2.4	28762	14	ACL64769 M. xanthu
C 90	44	2.4	110000	4	AAI99682_12
C 91	43.8	2.4	357	8	ABX49504 Bovine ES
92	43.8	2.4	1623	14	ACL65588 M. xanthu

c 93	43.8	2.4	1974	14	ACL68303	Ac168303 M. xanthu	166	42	2.3	3641	6	ABS76400	AbS76400 CDNA enco
c 94	43.8	2.4	2183	2	AAQ28290	AaQ28290 Fragment	167	42	2.3	3641	7	ADS73116	AdS73116 Human kid
c 95	43.8	2.4	27903	14	ACL64772	Ac164772 M. xanthu	168	42	2.3	3641	7	ADM41970	AdM41970 CDNA elev
c 96	43.6	2.4	682	6	ABL56817	Ab156817 Human hom	169	42	2.3	3641	9	ACC72416	AcC72416 Human ova
c 97	43.6	2.4	682	12	ADQ09870	AdQ09870 Human NK-	170	42	2.3	3641	13	ADN05013	AdN05013 Anticipori
c 98	43.6	2.4	682	12	ADQ09944	AdQ09944 Human NK-	171	42	2.3	3641	13	ADP25248	AdP25248 PRO polyp
c 99	43.6	2.4	1104	6	ABS54691	AbS54691 Human DNA	172	42	2.3	110000	4	AAI99682_11	AAI99682_11 o
c 100	43.6	2.4	2352	14	AEB91831	AeB91831 DNA enco	173	42	2.3	215974	12	ADQ97523	AdQ97523 Human can
c 101	43.6	2.4	3563	2	AAZ23429	AaZ23429 Human SCA	174	41.8	2.3	750	13	ADS63623	AdS63623 Bacterial
c 102	43.6	2.4	3596	2	AAV61588	AaV61588 Alpha-1A	175	41.8	2.3	777	13	ADT151588	AdT151588 Bacterial
c 103	43.6	2.4	3758	12	ADL06493	AdL06493 Human tum	176	41.8	2.3	1578	8	ACA40709	AcA40709 Bacterial
c 104	43.6	2.4	4670	12	ADQ17717	AdQ17717 Human sof	177	41.8	2.3	2515	11	ADN12368	AdN12368 Siah-1 ge
c 105	43.6	2.4	110000	4	AAI96882_08	AAI96882_08	178	41.8	2.3	23187	3	AAA50273	AAa50273 Human lep
c 106	43.6	2.4	110000	4	AAI96883_08	AAI96883_08	179	41.8	2.3	23187	3	AAI96882_30	AAI96882_30
c 107	43.6	2.4	14411	12	ADP74214	AdP74214 Equine he	180	41.8	2.3	110000	4	AAI96882_30	AAI96882_30
c 108	43.6	2.4	144486	12	ADP74215	AdP74215 Equine he	181	41.8	2.3	127722	12	ADQ97301	AdQ97301 Human can
c 109	43.6	2.4	145444	12	ADP74213	AdP74213 Equine he	182	41.8	2.3	1020	14	ACL69942	AcL69942 Lividans
c 110	43.6	2.4	145596	12	ADP74202	AdP74202 Equine he	183	41.6	2.3	1050	1	AAH80927	AAh80927 Plant ful
c 111	43.4	2.4	513	11	ACL34065	AcL34065 Rice abio	184	41.6	2.3	1054	13	ADX49671	AdX49671 Plant ful
c 112	43.4	2.4	1287	12	ADJ39845	AdJ39845 Plant CDN	185	41.6	2.3	1345	13	ADO84544	AdO84544 Plant ful
c 113	43.2	2.4	783	8	ACD05700	AcD05700 CDNA enco	186	41.6	2.3	1493	13	ADT17463	AdT17463 Plant CDN
c 114	43.2	2.4	1014	13	ADU01687	AdU01687 Novel hum	187	41.6	2.3	1822	13	ADT17463	AdT17463 Human DNA
c 115	43.2	2.4	1197	6	ABA96949	AbA96949 Human Sp1	188	41.6	2.3	1938	6	ABV78192	AbV78192 Human MTS
c 116	43.2	2.4	1249	4	ABL03433	AbL03433 Drosophil	189	41.6	2.3	1938	6	ABZ35768	AbZ35768 Human MTS
c 117	43.2	2.4	1304	4	ABL19259	AbL19259 Drosophil	190	41.6	2.3	1938	6	ABZ35768	AbZ35768 Human MTS
c 118	43.2	2.4	1554	10	ADC30435	AdC30435 Human nov	191	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 119	43.2	2.4	1925	14	ADX83136	AdX83136 Human TEG	192	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 120	43.2	2.4	2000	11	ACL17652	AcL17652 Rice stre	193	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 121	43.2	2.4	2659	12	ADL16413	AdL16413 Human pro	194	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 122	43.2	2.4	4124	4	ABL03432	AbL03432 Drosophil	195	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 123	43.2	2.4	4359	4	ABL19258	AbL19258 Drosophil	196	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 124	43.2	2.4	4667	12	ADQ22939	AdQ22939 Human sof	197	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 125	43	2.4	1155	13	ADT17378	AdT17378 Plant CDN	198	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 126	43	2.4	1251	6	ABS64842	AbS64842 Human tum	199	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 127	43	2.4	1444	13	ADL18777	AdL18777 Plant CDN	200	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 128	43	2.4	2760	11	ADL17062	AdL17062 Gene enco	201	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 129	43	2.4	2779	8	ABZ34851	AbZ34851 Coding se	202	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 130	43	2.4	3450	12	ADL06832	AdL06832 Streptomy	203	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 131	42.8	2.4	957	8	ACA26376	AcA26376 Prokaryot	204	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 132	42.8	2.4	1534	13	ADT18650	AdT18650 Plant CDN	205	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 133	42.8	2.4	2506	13	ACN43097	AcN43097 Human dia	206	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 134	42.8	2.4	3918	12	ADQ86282	AdQ86282 Human tum	207	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 135	42.8	2.4	3918	13	ADQ87442	AdQ87442 Human tum	208	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 136	42.8	2.4	7665	11	ADM29293	AdM29293 Human nov	209	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 137	42.8	2.4	11000	10	ADL18767	AdL18767 Human dis	210	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 138	42.8	2.4	128978	6	ABK83459	AbK83459 Human cdn	211	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 139	42.8	2.4	128978	8	ADA54587	AdA54587 Human lfm	212	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 140	42.8	2.4	128978	13	ADR52994	AdR52994 Drug ther	213	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 141	42.8	2.4	128978	14	ADX07226	AdX07226 Cyclin-de	214	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 142	42.6	2.3	684	12	ACH91599	AcH91599 Human gen	215	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 143	42.4	2.3	1093	13	ADT18801	AdT18801 Plant CDN	216	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 144	42.4	2.3	1497	8	ACA23725	AcA23725 Prokaryot	217	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 145	42.4	2.3	1679	8	ABZ78139	AbZ78139 Human can	218	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 146	42.4	2.3	104096	13	ADX56092	AdX56092 Streptomy	219	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 147	42.4	2.3	130000	4	AAI96883_11	AAI96883_11	220	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 148	42.4	2.3	135005	12	ADQ19501	AdQ19501 Human sof	221	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 149	42.2	2.3	65	6	ABN55771	AbN55771 Mouse spl	222	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 150	42.2	2.3	1645	14	AEB67751	AeB67751 Rice geno	223	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 151	42.2	2.3	1664	13	ADX50425	AdX50425 Plant ful	224	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 152	42.2	2.3	2869	13	ADT19972	AdT19972 Plant CDN	225	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 153	42.2	2.3	11820	2	AAV18130	AaV18130 Human chr	226	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 154	42.2	2.3	22976	2	ABK83426	AbK83426 Genomic r	227	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 155	42.2	2.3	41936	6	ABL67924	AbL67924 Ovary can	228	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 156	42.2	2.3	76994	12	ADP64454	AdP64454 Sorangium	229	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 157	42	2.3	1471	10	ACD19338	AcD19338 CDNA enco	230	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 158	42	2.3	1485	3	AZ61590	Az61590 DNA enco	231	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 159	42	2.3	1485	3	AZ61593	Az61593 DNA enco	232	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 160	42	2.3	1511	4	AAF74776	AaF74776 Human DEC	233	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 161	42	2.3	1961	4	ADQ09827	AdQ09827 Rice SPF1	234	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 162	42	2.3	2004	8	ACA40440	AcA40440 Prokaryot	235	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 163	42	2.3	2304	6	ABT05457	AbT05457 DNA of NO	236	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 164	42	2.3	3521	10	ADC30675	AdC30675 Human nov	237	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS
c 165	42	2.3	3641	4	AAF74767	AaF74767 Human DEC	238	41.6	2.3	1938	6	ABX10011	AbX10011 Human MTS

ALIGNMENTS

RESULT 1

ADK41027
ID ADK41027 standard; DNA; 2961 BP.

AC ADK41027;

DT 06-MAY-2004 (first entry)

DE Novel human kinase gene #47.

KW cytostatic; immunomodulator; cardiac; neuroprotective; nootropic;
KW antiparkinsonian; virucide; antibacterial; fungicide; ophthalmological;
KW analgesic; hypotensive; immunosuppressive; kinase inhibitor; kinase;
KW cancer; peripheral nervous system; central nervous system;
KW Alzheimer's disease; Parkinson's disease; multiple sclerosis;
KW amyotrophic lateral sclerosis; viral infection; prion infection;
KW ocular disease; migraine; pain; sexual dysfunction; mood disorder;
KW attention disorder; cognition disorder; hypotension; hypertension;
KW psychotic disorder; neurological disorder; dyskinesia; gene; ds.
KW metabolic disorder; organ transplant rejection; enzyme; gene; ds.

OS Homo sapiens.

XX WO2003057841-A2.

XX 17-JUL-2003.

XX 31-DEC-2002; 2002WO-US041687.

XX 31-DEC-2001; 2001US-0343169P.

XX (GRIG/) GRIGORIEV I V.

PA (SUDA/) SUDARSANAM S.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 13:46:36 ; Search time 9121.5 Seconds
(without alignments)
11329.436 Million cell updates/sec

Title: US-10-073-123-1

Perfect score: 1818

Sequence: 1 atggcggggctgtactgcgt.....aaactgtgtgttgcgtga 1818

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1818	100.0	1818	6	AX662143 Sequence
2	1818	100.0	2902	8	BC016480 Homo sapi
3	1818	100.0	2973	6	AX662145 Sequence
4	1818	100.0	2973	6	AX777280 Sequence
5	1818	100.0	2973	8	HSU78305 Sequence
6	1816.4	99.9	2865	8	BC033893 Homo sapi
7	1816.4	99.9	3001	8	BC060877 Homo sapi
8	1816	99.9	1818	8	BT009780 Homo sapi
9	1816	99.9	1818	11	AY888848 Homo sapi
10	1816	99.9	1818	11	AY888849 Synthetic
11	1739.2	95.7	2169	8	AB168475 Macaca fa
12	1697	93.3	3070	8	BC042418 Homo sapi
13	1380	75.9	1968	9	AF200464 Mus muscu
14	1378.4	75.8	2908	8	BC051966 Mus muscu
15	1367.2	75.2	2023	9	BC023492 Mus muscu
16	615.4	33.9	876	5	CR406758 Gallus ga
17	560	30.8	160854	8	AC110602 Homo sapi
18	560	30.8	174711	14	AC025515 Homo sapi

19	560	30.8	185101	14	AC079202
20	551.8	30.4	5840	5	BC072934
21	535	29.4	5223	5	BC044985
22	472.4	26.0	32601	8	AC111155
23	472.4	26.0	153922	8	AC111921
24	436	24.0	1909	5	BC085539
25	428.8	23.6	2469	5	BC066440
26	427.6	23.5	110000	14	AC107119
27	427.6	23.5	155813	14	AC136545
28	427.6	23.5	243587	14	AC106918
29	423.2	23.3	130030	9	BC323026
30	417.6	23.0	1829	5	BC045471
31	358.8	19.7	1347	6	C0732380
32	286	15.7	571	6	C0732300
33	278.8	15.3	110000	14	AC119019
34	248.2	13.7	2072	2	AK116603
35	230	12.7	174711	14	AC025515
36	208	11.4	155813	14	AC136545
37	172.6	9.5	5171	2	DMU96697
38	171	9.4	4901	6	C0577698
39	171	9.4	4901	6	AX777278
40	171	9.4	5259	2	AY069593
41	137.2	7.5	698	5	CR388740
42	136.6	7.5	222888	5	AL928954
43	135	7.4	168608	5	BX942836
44	134	7.4	183847	5	AC145510
45	134	7.4	192556	5	AC145764
46	118.4	6.5	148279	14	CR848825
47	118.4	6.5	174646	5	AL929151
48	105	5.8	606	6	C0747522
49	99.2	5.5	8256	6	C0577697
50	99.2	5.5	46607	14	AC013865
51	99.2	5.5	96924	14	DMBR2123
52	99.2	5.5	160629	2	AC023715
53	99.2	5.5	310993	2	AE003431
54	62	3.4	62	6	C0876234
55	61.4	3.4	125020	8	AF429315
56	60	3.3	60	6	C0541933
57	60	3.3	60	6	C0561689
58	60	3.3	60	6	C0561690
59	60	3.3	60	6	C0561946
60	57.6	3.2	2000	6	AX655393
61	57.4	3.2	186752	8	AC111200
62	57.2	3.1	216449	14	AC051616
63	56.4	3.1	160197	8	AP004221
64	55	3.0	163218	8	AC005837
65	54.6	3.0	125020	8	AF429315
66	53.6	2.9	144000	8	AC123764
67	53.4	2.9	193589	8	AC025370
68	53.4	2.9	347253	8	AF363578
69	52.8	2.9	170118	8	AC012384
70	52.6	2.9	2974	6	A41272
71	52.2	2.9	65225	14	AC079109
72	52	2.9	154037	8	AC072054
73	52	2.9	237479	14	AC156413
74	51.8	2.8	2337	4	AY138839
75	51.8	2.8	166118	4	CT009560
76	51.8	2.8	177412	14	CR974565
77	51.8	2.8	208220	8	AC009107
78	51.6	2.8	110000	15	AP008209
79	51.6	2.8	171442	15	AC125471
80	51.2	2.8	15738	6	AX803762
81	51.2	2.8	61944	6	AX803750
82	51	2.8	3177	8	AF055989
83	51	2.8	123149	8	AC008655
84	51	2.8	136753	14	AC149968
85	50.8	2.8	32329	1	SCA421798
86	50.8	2.8	118540	14	AC155485
87	50.8	2.8	162447	8	AC123886
88	50.4	2.8	110000	1	AE000516
89	50.4	2.8	316050	1	BX248346
90	50.4	2.8	349606	1	BX842583
91	50.2	2.8	154728	8	AC018730

C 92	49.8	2.7	2837	8	HSCGGL6P5	AJ001218 Homo sapi	C 165	47.2	2.6	161719	1	AY899214	AY899214 Streptomy
C 93	49.6	2.7	135171	14	AC120056	AC120056 Homo sapi	C 166	47.2	2.6	164051	6	C0875911	C0875911 Sequence
C 94	49.6	2.7	140126	8	AC141424	AC141424 Homo sapi	C 167	47	2.6	2000	6	AX654992	AX654992 Sequence
C 95	49.6	2.7	196050	1	AL646058	AL646058 Ralstonia	C 168	47	2.6	110000	15	AP008216	Continuation (160
C 96	49.6	2.7	199102	8	AC129507	AC129507 Homo sapi	C 169	47	2.6	110000	15	AP008208	Continuation (264
C 97	49.4	2.7	8113	13	HSBBICPAA	LI4320 Bovine herp	C 170	47	2.6	135098	15	AP0087549	AP0087549 Oryza sat
C 98	49.4	2.7	110000	15	AP008217_003	Continuation (4 of	C 171	47	2.6	136150	15	AP002485	AP002485 Oryza sat
C 99	49.4	2.7	135301	13	BHVLCGEN	LI4320 Bovine herp	C 172	47	2.6	161938	8	CNS0180Y	AL109769 Human chr
C 100	49.4	2.7	135301	13	BHVLCGEN	AJ004801 Bovine he	C 173	47	2.6	162227	14	AC024129	AC024129 Oryza sat
C 101	49.4	2.7	138032	14	AC141033	AJ004801 Bovine he	C 174	47	2.6	174019	15	AC087543	AC087543 Oryza sat
C 102	49.4	2.7	140116	14	AC158284	AC14033 Rattus no	C 175	47	2.6	303855	1	AE017230	AE017230 Mycobacte
C 103	49.4	2.7	164143	15	CNS08CDN	AC158284 Dromaeus	C 176	47	2.6	304748	15	AE017101	AE017101 Oryza sat
C 104	49.2	2.7	108964	15	AP0073391	AX000497 Oryza sat	C 177	46.8	2.6	168912	14	CR925779	CR925779 Danio rer
C 105	49.2	2.7	110000	15	AP008216_154	AC073391 Oryza sat	C 178	46.8	2.6	172658	14	AC141461	AC141461 Homo sapi
C 106	49.2	2.7	147321	14	AC155556	Continuation (155	C 179	46.8	2.6	176069	8	AC009452	AC009452 Homo sapi
C 107	49.2	2.7	165158	8	AC109815	AC155556 Zea mays	C 180	46.8	2.6	72639	14	AC068245	AC068245 Homo sapi
C 108	49.2	2.7	187718	8	AC104581	AC109815 Homo sapi	C 181	46.6	2.6	110000	15	AP008218	Continuation (235
C 109	49.2	2.7	300029	15	AE017099	AC104581 Homo sapi	C 182	46.6	2.6	110000	15	AP008211	Continuation (156
C 110	49	2.7	3875	1	SC78	AE017099 Oryza sat	C 183	46.6	2.6	110000	15	AP008213	Continuation (110
C 111	49	2.7	4536	1	SC016674	Y16674 Streptomyce	C 184	46.6	2.6	110000	15	AP008213_110	Continuation (111
C 112	49	2.7	110000	15	AP008209_247	Continuation (248	C 185	46.6	2.6	126544	15	AP005106	AP005106 Oryza sat
C 113	49	2.7	138390	13	AY261359	AY261359 Bovine he	C 186	46.6	2.6	136942	15	AC144739	AC144739 Oryza sat
C 114	49	2.7	138390	13	AY261359	AY261359 Bovine he	C 187	46.6	2.6	149732	14	AC143281	AC143281 Macaca mu
C 115	49	2.7	142014	14	CR407553	CR407553 Danio rer	C 188	46.6	2.6	162261	15	CNS08C88	AL731784 Oryza sat
C 116	49	2.7	143773	8	AC005631	AC005631 Homo sapi	C 189	46.6	2.6	172477	14	AY707984	AY707984 Oryza sat
C 117	49	2.7	159977	14	CR352334	CR352334 Danio rer	C 190	46.6	2.6	186825	8	AC149234	AC149234 Pan trogl
C 118	49	2.7	171518	14	AC120531	AC120531 Oryza sat	C 191	46.4	2.6	688	6	BD195611	BD195611 70 human
C 119	49	2.7	183327	15	CNS07IFP7	AL713930 Oryza sat	C 192	46.4	2.6	688	6	CQ775656	CQ775656 Sequence
C 120	49	2.7	321250	1	SC093911	AL939111 Streptomy	C 193	46.4	2.6	688	6	AR352666	AR352666 Sequence
C 121	48.4	2.7	1527	15	AK064271	AK064271 Oryza sat	C 194	46.4	2.6	688	6	AR650276	AR650276 Sequence
C 122	48.4	2.7	3059	15	AK069509	AK069509 Oryza sat	C 195	46.4	2.6	48498	15	AC091776	AC091776 Chlamydom
C 123	48.4	2.7	110000	15	AP008207_219	Continuation (220	C 196	46.4	2.6	111496	8	AC069351	AC069351 Homo sapi
C 124	48.4	2.7	110000	15	AP008208_261	Continuation (262	C 197	46.4	2.6	141578	4	AC092728	AC092728 Canis fam
C 125	48.4	2.7	132535	15	AP003308	AP003308 Oryza sat	C 198	46.4	2.6	168794	15	AC087726	AC087726 Chlamydom
C 126	48.4	2.7	146874	15	AP004868	AP004868 Oryza sat	C 199	46.4	2.6	208936	14	AC010821	AC010821 Homo sapi
C 127	48.4	2.7	203412	14	AC092961	AC092961 Homo sapi	C 200	46.2	2.5	1279	10	PM2H12G	AL684840 Penicilli
C 128	48.2	2.7	570	8	AH005569S01	AF012603 Homo sapi							
C 129	48.2	2.7	708	15	AK109263	AK109263 Oryza sat							
C 130	48.2	2.7	13695	8	HSU48436	U48436 Homo sapien							
C 131	48.2	2.7	110000	15	AP008216_195	Continuation (196							
C 132	48.2	2.7	135789	15	AC051634	AC051634 Oryza sat							
C 133	48.2	2.7	300029	15	AE017112	AE017112 Oryza sat							
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C 135	48	2.6	1393	10	PM11H12G	AL684264 Penicilli							
C 136	48	2.6	87471	8	AC041005	AC041005 Homo sapi							
C 137	48	2.6	104581	14	AF267908	AF267908 Homo sapi							
C 138	48	2.6	110000	15	AP008217_001	Continuation (2 of							
C 139	48	2.6	110000	15	AP008218_001	Continuation (2 of							
C 140	48	2.6	160673	15	CNS08CDR	BX000501 Oryza sat							
C 141	48	2.6	161808	15	CNS08CDR	AX000496 Oryza sat							
C 142	48	2.6	165028	9	AC102794	AC102794 Mus muscu							
C 143	48	2.6	172475	14	AC154766	AC154766 Mus muscu							
C 144	48	2.6	175114	14	AC165944	AC165944 Mus muscu							
C 145	47.8	2.6	444	6	CQ984093	CQ984093 Sequence							
C 146	47.8	2.6	110000	1	AP006618_53	Continuation (54 o							
C 147	47.8	2.6	127407	14	AC146863	AC146863 Medicago							
C 148	47.8	2.6	179825	14	AC009672	AC009672 Homo sapi							
C 149	47.8	2.6	184503	14	AC140624	AC140624 Macaca mu							
C 150	47.8	2.6	259023	14	AC108591	AC108591 Rattus no							
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C 152	47.6	2.6	192814	8	AC007597	AC007597 Homo sapi							
C 153	47.6	2.6	276326	15	AY574035	AY574035 Zea mays							
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C 156	47.4	2.6	179047	15	AP005838	AP005838 Oryza sat							
C 157	47.4	2.6	184759	15	AP005702	AP005702 Oryza sat							
C 158	47.4	2.6	250583	14	AC152089	AC152089 Bos tauru							
C 159	47.2	2.6	3163	8	BC066776	BC066776 Homo sapi							
C 160	47.2	2.6	15624	6	CQ875923	CQ875923 Sequence							
C 161	47.2	2.6	98876	8	AC009488	AC009488 Homo sapi							
C 162	47.2	2.6	131329	8	AC004873	AC004873 Homo sapi							
C 163	47.2	2.6	144656	8	AC021573	AC021573 Homo sapi							
C 164	47.2	2.6	157435	8	HS50024	AL034380 Human DNA							

ALIGNMENTS

RESULT 1

AX662143

LOCUS

AX662143

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

ORIGIN

Query Match

Best Local Similarity

Matches 1818;

Qy

Db

AX662143

Sequence 1 from Patent WO02064838.

AX662143

AX662143.1

GI:29163065

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

Li, J. and Powers, S.

Amplified cancer gene wipl

Patent: WO 02064838-A 1 22-AUG-2002;

Tularik Inc. (US)

Location/Qualifiers

1. .1818

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

100.0%; Score 1818; DB 6; Length 1818;

100.0%; Pred. No.: 0;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||

1 ATGGCGGGCTGTACTCGCTGGGAGTACGCTTTCTCCGACCGAGGCGGAGGAAGTAC 60